SEQUENCE LISTING

<110> NEXIMMUNE
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<120> COMPOSITIONS AND METHODS FOR IMMUNOTHERAPY

<130> NEX-001PC

<140> PCT/US2014/043629
<141> 2014-06-23

<150> US 61/838,547
<151> 2013-06-24

<150> US 61/948,916
<151> 2014-03-06

<160> 34

<170> PatentIn version 3.5

<210> 1
<211> 360
<212> DNA
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<220>
<223> Synthetic sequence (Humanized variable heavy sequence for anit-CD28)

<220>
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<222> (1)..(360)

<400> 1

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gag gtg aag ctg cag cag tca gga cct ggc ctg gtg aag ccc tca gag          48
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                  10                  15

acc ctg tcc ctc act tgt act gtc tct ggg ttt tca tta agc gac tat          96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

ggt gtt cat tgg gtt cgc cag gct cca gga aag gga ctg gag tgg ctg         144
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg         192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga aag acc atc agc aaa gac aac tcc aag agc caa gtt ttc tta         240
Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80

aaa atg aac agt ctg aca gct gct gac aca gcc gtg tat tac tgt gcc         288
Lys Met Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc tat tac tat tct atg gac tac tgg ggc caa         336
Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                        360
```

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 2
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Anti-CD28 VH2)

<220>
<221> CDS
<222> (1)..(360)

<400> 3
gag gtg aag ctg cag cag tca gga cct ggc ctg gtg aag ccc tca gag 48
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc act tgt act gtc tct ggg ttt tca tta agc gac tat 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
20 25 30

```
ggt gtt cat tgg gtt cgc cag gct cca gga aag gga ctg gag tgg ctg        144
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg        192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga aag acc atc agc aaa gac aac tcc aag agc caa gtt tcc tta        240
Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

aaa atg agc agt gtg aca gct gct gac aca gcc gtg tat tac tgt gcc        288
Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc tat tac tat tct atg gac tac tgg ggc caa        336
Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                       360
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 4
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4

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Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 5

<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence ((Anti-CD28 VH3)

<220>
<221> CDS
<222> (1)..(360)

<400> 5

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gag gtg aag ctg cag cag tca gga cct ggc ctg gtg aag ccc tca gag          48
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

acc ctg tcc ctc act tgt act gtc tct ggg ttt tca tta agc gac tat          96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

ggt gtt cat tgg gtt cgc cag gct cca gga aag gga ctg gag tgg ctg         144
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg         192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga gtg acc atc agc aaa gac aac tcc aag agc caa gtt tcc tta         240
Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

aaa ctg agc agt gtg aca gct gct gac aca gcc gtg tat tac tgt gcc         288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc tat tac tat tct atg gac tac tgg ggc caa         336
Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                        360
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 6
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
```

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 7
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Anti-CD28 VK1)

<220>
<221> CDS
<222> (1)..(333)

<400> 7
gac atc gag ctc act cag tct cca gat tct ttg gct gtg tct cta ggg 48
Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag aga gcc acc atc aac tgc aga gcc agt gag agt gtt gaa tat tat 96
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

gtc aca agt tta atg cag tgg tac cag cag aag cca gga cag cca ccc 144
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

aaa ctc ctc atc ttt gct gca tcc aac gta gaa tct ggg gtc cct gac 192
Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
50 55 60

agg ttt agt ggc agt ggg tct ggg aca aac ttc acc ctc acc atc tct 240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65 70 75 80

tct ctg cag gag gag gat gtt gca atg tat ttc tgt cag caa agt agg 288
Ser Leu Gln Glu Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

aag gtt cct tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa 333
Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 8
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Glu Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 9
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Anti-CD28 VK2)

<220>
<221> CDS
<222> (1)..(333)

<400> 9
gac atc gag ctc act cag tct cca gat tct ttg gct gtg tct cta ggg 48
Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag aga gcc acc atc aac tgc aga gcc agt gag agt gtt gaa tat tat 96
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

gtc aca agt tta atg cag tgg tac cag cag aag cca gga cag cca ccc 144
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

aaa ctc ctc atc ttt gct gca tcc aac gta gaa tct ggg gtc cct gac 192
Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
50 55 60

agg ttt agt ggc agt ggg tct ggg aca aac ttc acc ctc acc atc tct 240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65 70 75 80

tct ctg cag gcc gag gat gtt gca atg tat ttc tgt cag caa agt agg 288

Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

aag gtt cct tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa 333
Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 10
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 10

Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 11
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Anti-CD28 VK3)

<220>
<221> CDS
<222> (1)..(333)

<400> 11
gac atc gag ctc act cag tct cca gat tct ttg gct gtg tct cta ggg 48
Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag aga gcc acc atc aac tgc aga gcc agt gag agt gtt gaa tat tat 96
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

```
gtc aca agt tta atg cag tgg tac cag cag aag cca gga cag cca ccc      144
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

aaa ctc ctc atc ttt gct gca tcc aac gta gaa tct ggg gtc cct gac      192
Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
    50                  55                  60

agg ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc acc atc tct      240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80

tct ctg cag gcc gag gat gtt gca atg tat ttc tgt cag caa agt agg      288
Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
                85                  90                  95

aag gtt cct tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa          333
Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```

<210> 12
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

```
Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
            20                  25                  30

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80

Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
                85                  90                  95

Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```

<210> 13
<211> 984
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (modified constant heavy sequence)

<220>
<221> CDS
<222> (1)..(984)

<400> 13

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gct tcc acc aag ggc cca tcc gtc ttc ccc ctg gcg ccc tgc tcc agg          48
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

agc acc tcc gag agc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac          96
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc         144
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc         192
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acg aag acc         240
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

tac acc tgc aat gta gat cac aag ccc agc aac acc aag gtg gac aag         288
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

aga gtt gag tcc aaa tat ggt ccc cca tgc cca cca tgc cca gca cct         336
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

gag ttc gag ggg gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag         384
Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

gac act ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg gtg         432
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

gac gtg agc cag gaa gac ccc gag gtc cag ttc aac tgg tac gtg gat         480
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag ttc         528
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac         576
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa ggc ctc         624
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

ccg tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga         672
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

gag cca cag gtg tac acc ctg ccc cca tcc cag gag gag atg acc aag         720
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac         768
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
```

```
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag          816
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc          864
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

agg cta acc gtg gac aag agc agg tgg cag gag ggg aat gtc ttc tca          912
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

tgc tcc gtg atg cat gag gct ctg cac aac cac tac aca cag aag agc          960
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

ctc tgc ctg tct ctg ggt aaa tga                                          984
Leu Cys Leu Ser Leu Gly Lys
                325
```

<210> 14
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140
```

```
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Cys Leu Ser Leu Gly Lys
                325
```

<210> 15
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (constant k Light sequence)

<220>
<221> CDS
<222> (1)..(324)

<400> 15

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cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag          48
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc          96
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
```

20 25 30

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 144
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 192
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 240
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 288
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

ccc gtc aca aag agc ttc aac agg gga gag tgt tag 324
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 16
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 17
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (humanized non-CD28-binding variable region)

<220>
<221> CDS
<222> (1)..(360)

<400> 17

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gag gtg aag ctg cag cag tca gga cct ggc ctg gtg aag ccc tca gag          48
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

acc ctg tcc ctc act tgt act gtc tct ggg ttt aca ttc agc gac tat          96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

ggt gtt cat tgg att cgc cag cct cca gga aag gga ctg gag tgg atc         144
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg         192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga gtg acc atc agc gtg gac acc tcc aag aac caa ttt tcc tta         240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

aaa ctg agc agt gtg aca gct gct gac aca gcc gtg tat tac tgt gcc         288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc gct gcc gct tct atg gac tac tgg ggc caa         336
Arg Asp Lys Gly Tyr Ser Ala Ala Ala Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                        360
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 18
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

```
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80
```

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Lys Gly Tyr Ser Ala Ala Ala Ser Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 19
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence (humanized HLA-IgG4HC)

<400> 19

Gln Val Gln Leu Thr Arg Glu Gly Ser Gly Ser His Ser Met Arg Tyr
1 5 10 15

Phe Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile
20 25 30

Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp
35 40 45

Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu
50 55 60

Gly Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser
65 70 75 80

Gln Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln
85 90 95

Ser Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val
100 105 110

Gly Ser Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp
115 120 125

Gly Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala
130 135 140

Ala Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His
145 150 155 160

Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp
165 170 175

Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp
180 185 190

Ala Pro Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala
195 200 205

Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu
210 215 220

Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val
225 230 235 240

Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
245 250 255

Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His
260 265 270

Glu Gly Leu Pro Lys Pro Leu Thr Trp Ala Arg Glu Val Ser Glu Val
275 280 285

Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
290 295 300

Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Ser Asp Tyr Gly Val
305 310 315 320

His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val
325 330 335

Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg
340 345 350

Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu
355 360 365

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
370 375 380

Lys Gly Tyr Ser Ala Ala Ala Ser Met Asp Tyr Trp Gly Gln Gly Thr
385 390 395 400

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
405 410 415

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
420 425 430

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
435 440 445

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
450 455 460

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
465 470 475 480

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
485 490 495

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
500 505 510

Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu
515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
530 535 540

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
565 570 575

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
595 600 605

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625 630 635 640

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
675 680 685

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
690 695 700

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705 710 715 720

His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
725 730

<210> 20
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Light Chain 3 (LC3 or Vk3))

<400> 20

Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 21
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Heavy Chain 1 (HC1))

<400> 21

Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
435 440 445

<210> 22
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Heavy Chain 2 (HC2))

<400> 22

Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65 70 75 80

Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
435 440 445

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 23

Asp Tyr Gly Val His
1 5

<210> 24
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 24

Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met Ser
1 5 10 15

<210> 25
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 25

Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr
1 5 10

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 26

Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln
1 5 10 15

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 27

Ala Ala Ser Asn Val Glu Ser
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 28

Gln Gln Ser Arg Lys Val Pro Tyr Thr
1 5

<210> 29
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 29

Gly Gly Gly Ser Gly
1 5

<210> 30
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 30

Ala Ala Ala Gly Gly
1 5

<210> 31
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (N-terminal linker)

<220>
<221> CDS
<222> (1)..(51)

<400> 31
cag gtc caa ctg acg cgt gag ggg tcc ggc tct cac tcc atg agg tat 48
Gln Val Gln Leu Thr Arg Glu Gly Ser Gly Ser His Ser Met Arg Tyr
1 5 10 15

ttc 51
Phe

<210> 32
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

Gln Val Gln Leu Thr Arg Glu Gly Ser Gly Ser His Ser Met Arg Tyr
1 5 10 15

Phe

<210> 33
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (C-terminal linker)

<220>
<221> CDS
<222> (1)..(57)

<400> 33
gag ggt ttg ccc aag ccc ctc acc tgg gct cga gag gtg agc gag gtc 48
Glu Gly Leu Pro Lys Pro Leu Thr Trp Ala Arg Glu Val Ser Glu Val
1 5 10 15

aag ctg cag 57
Lys Leu Gln

<210> 34
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

Glu Gly Leu Pro Lys Pro Leu Thr Trp Ala Arg Glu Val Ser Glu Val
1 5 10 15

Lys Leu Gln